



PCT10

RAW SEQUENCE LISTING

DATE: 02/07/2002

PATENT APPLICATION: US/10/031,014

TIME: 16:15:28

Input Set : A:\20493p.txt

Output Set: N:\CRF3\02072002\J031014.raw

ENTERED

4 <110> APPLICANT: Howard, Andrew D.
 6 <120> TITLE OF INVENTION: Melanin-Concentrating Hormone Receptor
 9 <130> FILE REFERENCE: 20493P
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/031,014
 C--> 11 <141> CURRENT FILING DATE: 2002-01-10
 11 <150> PRIOR APPLICATION NUMBER: PCT/US00/18733
 12 <151> PRIOR FILING DATE: 2000-07-10
 14 <150> PRIOR APPLICATION NUMBER: US 60/143,706
 15 <151> PRIOR FILING DATE: 1999-07-14
 17 <160> NUMBER OF SEQ ID NOS: 10
 19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1062
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Human
 26 <400> SEQUENCE: 1
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 28 cccgataacc tcacttcggc aggatcacct cctcgcacgg ggagcatctc ctacatcaac 120
 29 atcatcatgc cttcgggtgt cggcaccatc tgccctcctgg gcatcatcgg gaactccacg 180
 30 gtcattctcg cggtcgtgaa gaagtccaag ctgcactggg gcaacaacgt ccccgacatc 240
 31 ttcatcatca acctctcggg agtagatctc ctctttctcc tgggcatgcc ctcatgatc 300
 32 caccagctca tgggcaatgg ggtgtggcac tttggggaga ccatgtgcac cctcatcacg 360
 33 gccatggatg ccaatagtca gttcaccagc acctacatcc tgaccgccat ggccattgac 420
 34 cgctacctgg ccaactgtcca ccccatctct tccacgaagt tccggaagcc ctctgtggcc 480
 35 accctggtga tctgcctcct gtggggccctc tccttcatca gcatcacccc tgtgtggctg 540
 36 tatgccagac tcatcccctt cccaggaggt gcagtgggct gcggcatacg cctgcccac 600
 37 ccagacactg acctctactg gttcaccctg taccagtttt tcctggcctt tgccctgcct 660
 38 tttgtggtca tcacagccgc atactgtagg atcctgcagc gcatgacgtc ctcatgtggc 720
 39 cccgcctccc agcgcagcat ccggctgcgg acaaagaggg tgaccgcgac agccatcgcc 780
 40 atctgtctgg tcttctttgt gtgctgggca ccctactatg tgctacagct gaccagttg 840
 41 tccatcagcc gcccgaccct cacccttgtc tacttataca atgcggccat cagcttgggc 900
 42 tatgccaaca gctgcctcaa cccctttgtg tacatcgtgc tctgtgagac gttccgcaaa 960
 43 cgcttggtcc tgtcgtgaa gcctgcagcc caggggcagc ttcgcgctgt cagcaacgct 1020
 44 cagacggctg acgaggagag gacagaaagc aaaggcacct ga 1062
 46 <210> SEQ ID NO: 2
 47 <211> LENGTH: 353
 48 <212> TYPE: PRT
 49 <213> ORGANISM: Human
 51 <400> SEQUENCE: 2
 52 Met Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly Pro Asn Ala Ser Asn
 53 1 5 10 15
 54 Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala Gly Ser Pro Pro Arg
 55 20 25 30

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56 Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly
57          35          40          45
58 Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser Thr Val Ile Phe Ala
59          50          55          60
60 Val Val Lys Lys Ser Lys Leu His Trp Cys Asn Asn Val Pro Asp Ile
61 65          70          75          80
62 Phe Ile Ile Asn Leu Ser Val Val Asp Leu Phe Leu Leu Gly Met
63          85          90          95
64 Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly
65          100          105          110
66 Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe
67          115          120          125
68 Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile Asp Arg Tyr Leu Ala
69          130          135          140
70 Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Val Ala
71 145          150          155          160
72 Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr
73          165          170          175
74 Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val
75          180          185          190
76 Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe
77          195          200          205
78 Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile
79          210          215          220
80 Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met Thr Ser Ser Val Ala
81 225          230          235          240
82 Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg
83          245          250          255
84 Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr
85          260          265          270
86 Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr
87          275          280          285
88 Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser
89          290          295          300
90 Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys
91 305          310          315          320
92 Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Ala
93          325          330          335
94 Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys Gly
95          340          345          350
96 Thr
99 <210> SEQ ID NO: 3
100 <211> LENGTH: 1254
101 <212> TYPE: DNA
102 <213> ORGANISM: Human
104 <400> SEQUENCE: 3
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106 gaggaagacc cccttcccaa ctgcggggct tgcgctccgg gacaaggtgg caggcgctgg      120
107 aggctgccgc agcctgcgtg ggtggagggg agctcagctc ggttgtggga gcaggcgacc      180

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108 ggcaactggct ggatggacct ggaagcctcg ctgctgccca ctggtcccaa cgccagcaac 240
109 acctctgatg gccccgataa cctcacttcg gcaggatcac ctctctgcac ggggagcatc 300
110 tcctacatca acatcatcat gccttcgggtg ttcggcacca tctgctcctt gggcatcatc 360
111 gggaactcca cggtcattctt cgcggctcgtg aagaagtcca agctgcaactg gtgcaacaac 420
112 gtccccgaca tcttcatcat caacctctcg gtagtagatc tctcttttct cctgggcatg 480
113 cccttcatga tccaccagct catgggcaat ggggtgtggc actttgggga gaccatgtgc 540
114 accctcatca cggccatgga tgccaatagt cagttcacca gcacctacat cctgaccgcc 600
115 atggccattg accgctacct ggccactgtc caccatctct cttccacgaa gttccggaag 660
116 ccctctgtgg ccaccctggg gatctgcctc ctgtggggccc tctccttcat cagcatcacc 720
117 cctgtgtggc tgtatgccag actcatcccc ttcccaggag gtgcagtggtg ctgcggcata 780
118 cgctgcccc acccagacac tgacctctac tggttcacc tgtaccagtt tttcctggcc 840
119 ttgcccctgc cttttgtggg catcacagcc gcatacgtga ggatcctgca gcgcatgacg 900
120 tctcagtggt cccccgcctc ccagcgcagc atccggctgc ggacaaagag ggtgaccgcc 960
121 acagccatcg ccattctgtt ggtcttcttt gtgtgctggg caccctacta tgtgctacag 1020
122 ctgaccatgt tgtccatcag ccgcccagcc ctcacctttg tctacttata caatgcggcc 1080
123 atcagcttgg gctatgccaa cagctgcctc aaccctttg tgtacatcgt gctctgtgag 1140
124 acgttcogca aacgcttggg cctgtcgggtg aagcctgcag cccaggggca gcttcgcgct 1200
125 gtcagcaacg ctcagacggc tgacgaggag aggcagagaa gcaaaggcac ctga 1254

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127 <210> SEQ ID NO: 4

128 <211> LENGTH: 417

129 <212> TYPE: PRT

130 <213> ORGANISM: Human

132 <400> SEQUENCE: 4

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133 Met Lys Lys Gly Val Gly Arg Ala Val Gly Leu Gly Gly Gly Ser Gly
134 1 5 10 15
135 Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asn Cys Gly Ala Cys Ala
136 20 25 30
137 Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro Gln Pro Ala Trp Val
138 35 40 45
139 Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala Thr Gly Thr Gly Trp
140 50 55 60
141 Met Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly Pro Asn Ala Ser Asn
142 65 70 75 80
143 Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala Gly Ser Pro Pro Arg
144 85 90 95
145 Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly
146 100 105 110
147 Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser Thr Val Ile Phe Ala
148 115 120 125
149 Val Val Lys Lys Ser Lys Leu His Trp Cys Asn Asn Val Pro Asp Ile
150 130 135 140
151 Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met
152 145 150 155 160
153 Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly
154 165 170 175
155 Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe
156 180 185 190
157 Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile Asp Arg Tyr Leu Ala
158 195 200 205

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159 Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Val Ala
160      210                      215                      220
161 Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr
162 225                      230                      235                      240
163 Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val
164                      245                      250                      255
165 Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe
166      260                      265                      270
167 Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile
168      275                      280                      285
169 Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met Thr Ser Ser Val Ala
170      290                      295                      300
171 Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg
172 305                      310                      315                      320
173 Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr
174                      325                      330                      335
175 Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr
176      340                      345                      350
177 Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser
178      355                      360                      365
179 Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys
180      370                      375                      380
181 Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Ala
182 385                      390                      395                      400
183 Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys Gly
184      405                      410                      415
185 Thr
188 <210> SEQ ID NO: 5
189 <211> LENGTH: 1269
190 <212> TYPE: DNA
191 <213> ORGANISM: Human
193 <400> SEQUENCE: 5
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195 ggctgccagg ctacggagga agacccctt cccaactgcg gggcttgccg tccgggacaa      120
196 ggtggcaggc gctggaggct gccgcagcct gcgtgggtgg aggggagctc agctcggttg      180
197 tgggagcagg cgaccggcac tggctggatg gacctggaag cctcgctgct gccactggt      240
198 cccaacgcca gcaacacctc tgatggcccc gataacctca cttcggcagg atcacctcct      300
199 cgcacgggga gcatctccta catcaacatc atcatgcctt cgggtgttcg caccatctgc      360
200 ctctctggga tcatcggaat ctccacggtc atcttcgcgg tcgtgaagaa gtccaagctg      420
201 cactggtgca acaacgtccc cgacatcttc atcatcaacc tctcggtagt agatctcctc      480
202 tttctcctgg gcatgccctt catgatccac cagctcatgg gcaatggggt gtggcacttt      540
203 ggggagacca tgtgcacctt catcacggcc atggatgcca atagtcagtt caccagcacc      600
204 tacatcttga ccgccatggc cattgaccgc tacctggcca ctgtccaccc catctcttcc      660
205 acgaagtccc ggaagccctc tgtggccacc ctgggtgatc gctcctgtg ggccctctcc      720
206 ttcacacgca tcaccctgt gtggctgtat gccagactca tcccttccc aggaggtgca      780
207 gtgggtgcg gccacgcct gcccaaccga gacactgacc tctactggtt caccctgtac      840
208 cagtttttcc tggcctttgc cctgcctttt gtggtcatca cagccgcata cgtgaggatc      900
209 ctgcagcgca tgacgtctc agtggccccc gctcccagc gcagcatccg gctgaggaca      960
210 aagagggtga cccgcacagc catcgccatc tgtctggtct tctttgtgtg ctgggcaccc      1020

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Output Set: N:\CRF3\02072002\J031014.raw

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211 tactatgtgc tacagctgac ccagttgtcc atcagccgcc cgaccctcac ctttgtctac 1080
212 ttatacaatg cggccatcag cttgggctat gccaacagct gcctcaaccc ctttgtgtac 1140
213 atcgtgctct gtgagacggt cgcgaaacgc ttggctctgt cggatgaagcc tgcagcccag 1200
214 gggcagcttc ggcgtgtcag caacgctcag acggctgacg aggagaggac agaaagcaaa 1260
215 ggcacctga 1269
217 <210> SEQ ID NO: 6
218 <211> LENGTH: 422
219 <212> TYPE: PRT
220 <213> ORGANISM: Human
222 <400> SEQUENCE: 6
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225 Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asn
226 20 25 30
227 Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro
228 35 40 45
229 Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
230 50 55 60
231 Thr Gly Thr Gly Trp Met Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
232 65 70 75 80
233 Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
234 85 90 95
235 Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met
236 100 105 110
237 Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser
238 115 120 125
239 Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn
240 130 135 140
241 Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu
242 145 150 155 160
243 Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly
244 165 170 175
245 Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp
246 180 185 190
247 Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile
248 195 200 205
249 Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg
250 210 215 220
251 Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser
252 225 230 235 240
253 Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe
254 245 250 255
255 Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr
256 260 265 270
257 Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu
258 275 280 285
259 Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met
260 290 295 300
261 Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/031,014

DATE: 02/07/2002

TIME: 16:15:29

Input Set : A:\20493p.txt

Output Set: N:\CRF3\02072002\J031014.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date